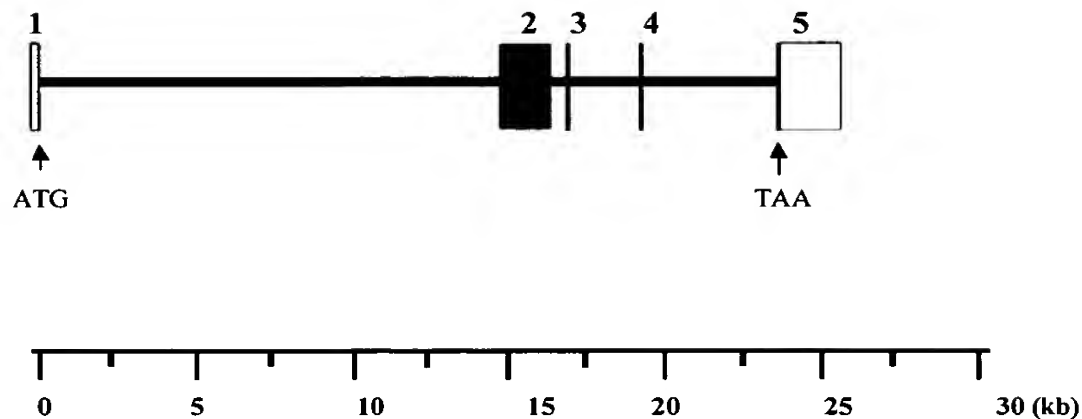


Fig. 1

A



B

EXON	EXON SIZE	3' SPLICE ACCEPTOR	5' SPLICE DONOR	INTRON SIZE
1	254		TCGCCATG G / gtaagtc Met G 1 2	15300
2	1284	tttttag / GC CAC TCC ly His Ser 2 3 4	GGG CCA G / gtaagtg Gly Pro V 428 429 4	538
3	123	accctag / TG ACC TGG al Thr Trp 30 431 432	CTC ATT G / gtgagtc Leu Ile G 469 470 4	2365
4	135	tttccag / GC ACC ATC ly Thr Ile 71 472 473	AAG AGA CG / gtaggaa Lys Arg Ar 514 515 516	4266
5	2849	ctgacag / G TTC ACC g Phe Thr 517 518	<u>AATAAAGAGTTTGT</u> TATTAATTTGT(A) ₃ ' UTR 2519	

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[illegible][illegible]

GLU110	GRRAVDFEATIGSSMAACICIVVSEELVGP	RVFVSVSEETVGGILTSYALINXALAGTP	WRHMFVEATAPPA	LDLSHLF	184
GLU78	GRRLTLVGLGAGVAAAGVAAAGVAAAGVAA	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	204
GLU75	ISRLTLVGLGAGVAAAGVAAAGVAAAGVAA	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	204
GLU74	LGRFLVGLGAGVAAAGVAAAGVAAAGVAA	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	215
GLU73	LGRFLVGLGAGVAAAGVAAAGVAAAGVAA	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	225
GLU72	AGRFITSLVGLGAGVAAAGVAAAGVAAAGV	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	237
GLU71	AGRFITSLVGLGAGVAAAGVAAAGVAAAGV	GLVGLVGLVGLVGLVGLVGLVGLVGLVGLV	WRHMFVEATAPPA	LDLSHLF	247

[illegible][illegible]

GLUT10	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	348	
GLUT8	Q	D	S	L	Q	D	S	L	P	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	349	
GLUT5	G	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	350
GLUT4	G	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	351
GLUT3	G	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	352
GLUT2	G	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	353
GLUT1	G	L	P	D	S	L	Q	D	S	L	P	P	P	R	I	N	E	D	Q	R	E	P	I	L	S	T	A	K	K	T	K	P	H	R	S	G	D	E	S	A	P	R	E	A	S	S	A	I	S	C	E	P	L	P	A	R	G	H	A	L	L	R	E	T	A	L	G	S	M	V	E	A	F	E	E	G	354

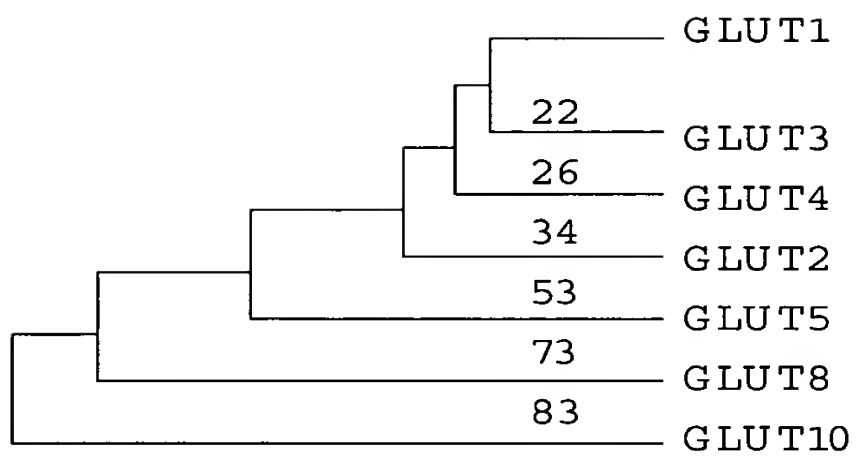
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GL0710	QZRRFTLGFGRQNS	TPY	SRIEISAAS	541
GL0709	EGR			477
GL0708	TKM			501
GL0707	HRTP	SL	EQEVEKSTELF	509
GL0706	EGOAHG	QEDGV	MEMNSIEPAKE	496
GL0705	QKQSG	SAHRE	KAAVEMKFLGA	524
GL0704	QKQSG	SAHRE	KAAVEMKFLGA	524
GL0703	QKQSG	SAHRE	KAAVEMKFLGA	524
GL0702	QKQSG	SAHRE	KAAVEMKFLGA	524
GL0701	QKQSG	SAHRE	KAAVEMKFLGA	524

FIG 2A

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Fig. 2B



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Fig. 3

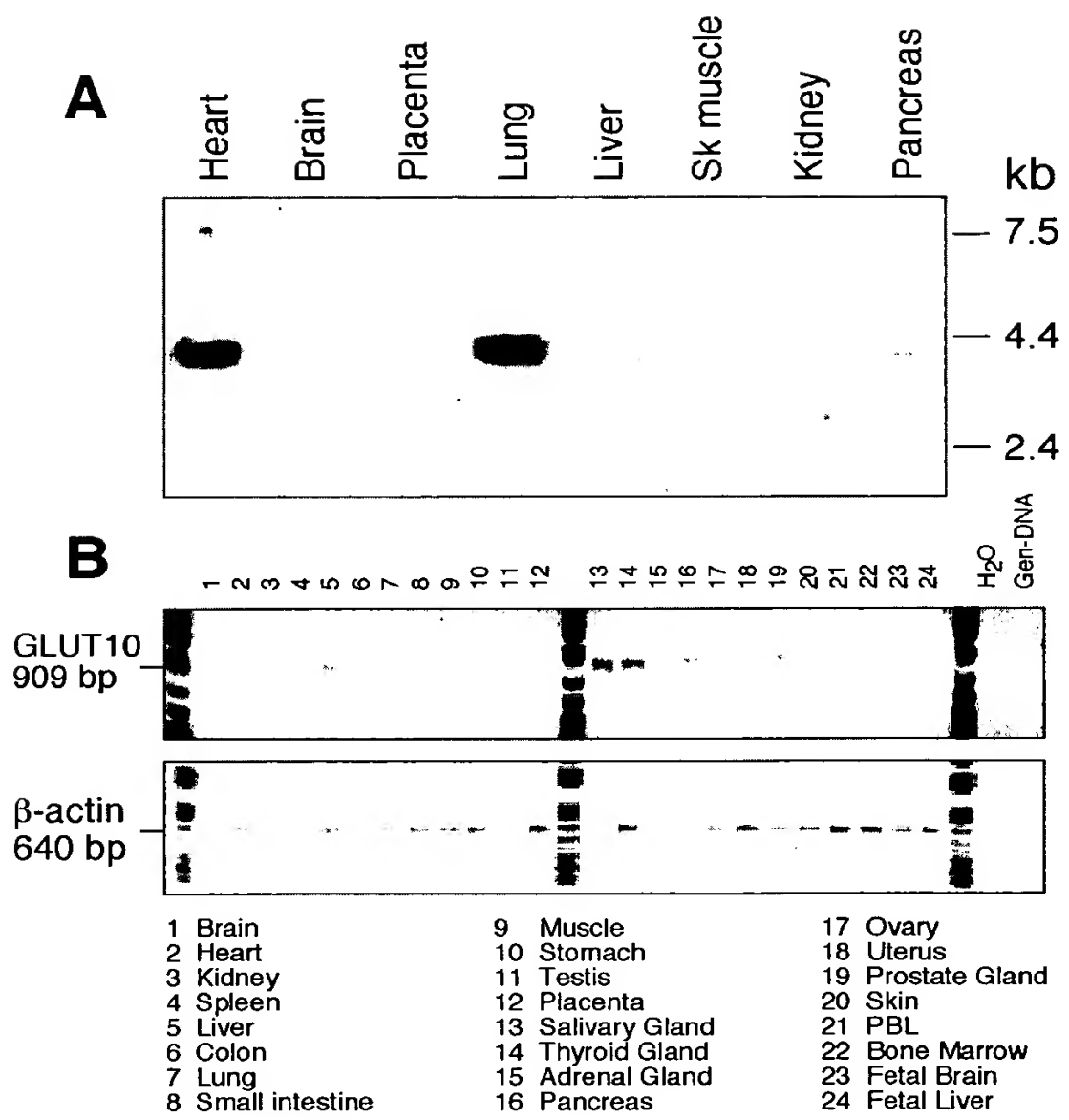
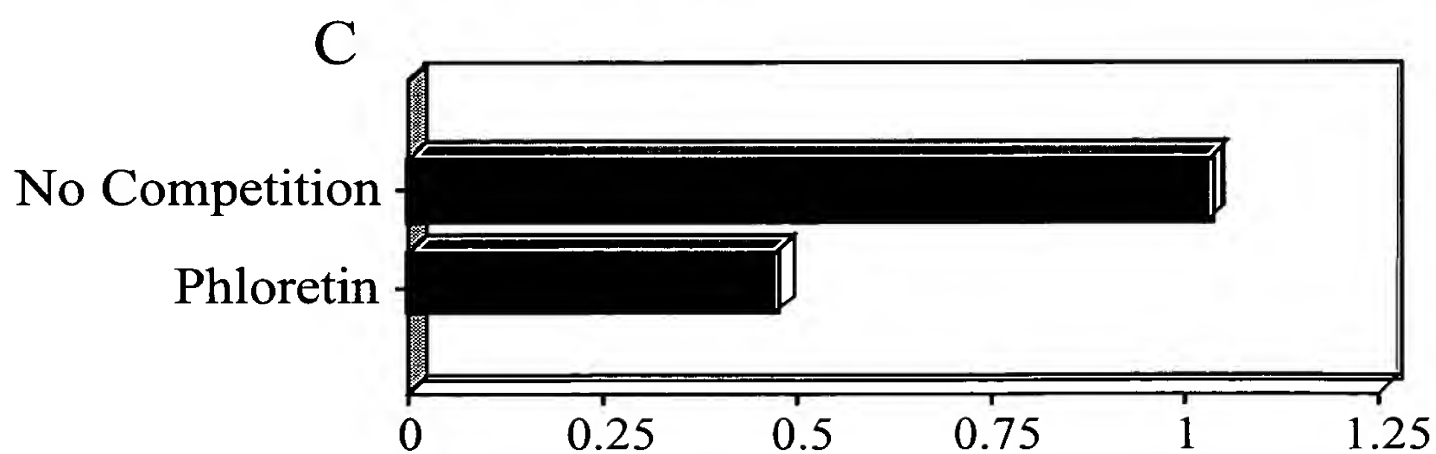
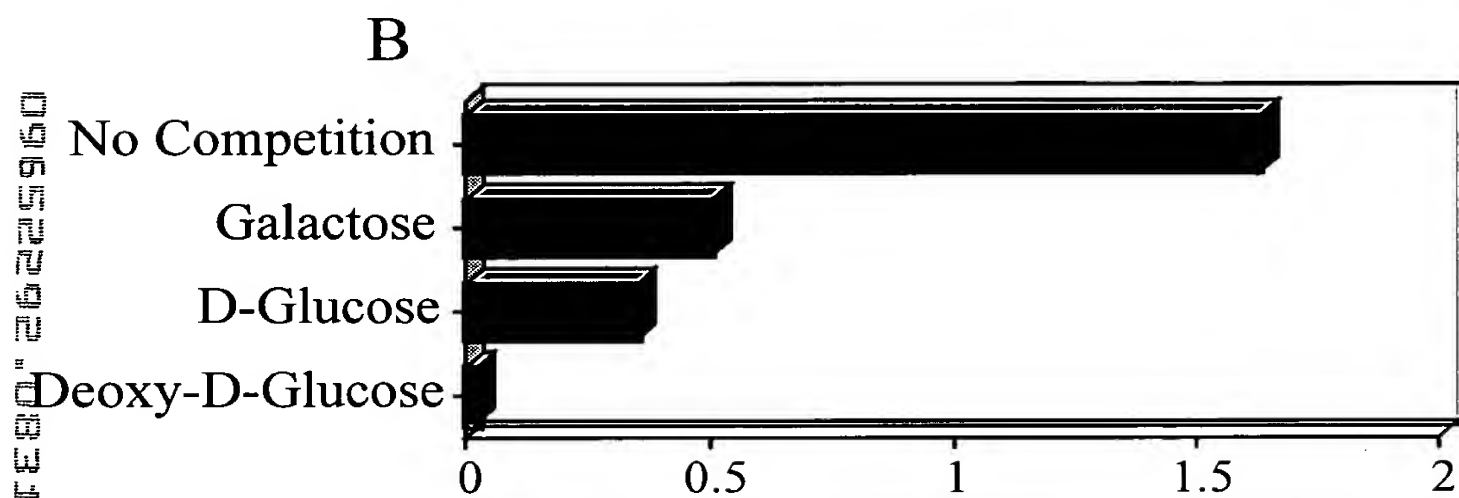
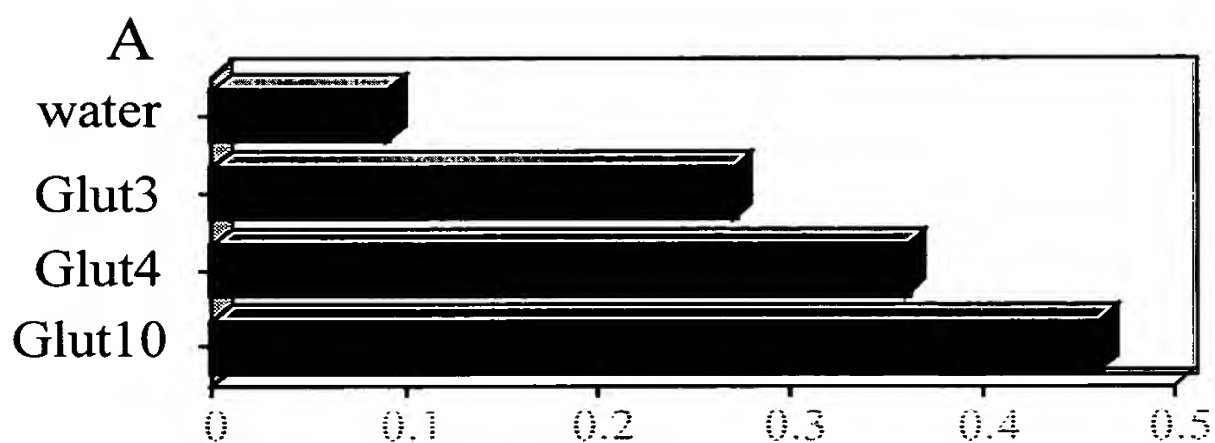


Fig. 4



2-Deoxy-D-Glucose Uptake
(pmol/oocyte/30 min)

Fig. 5

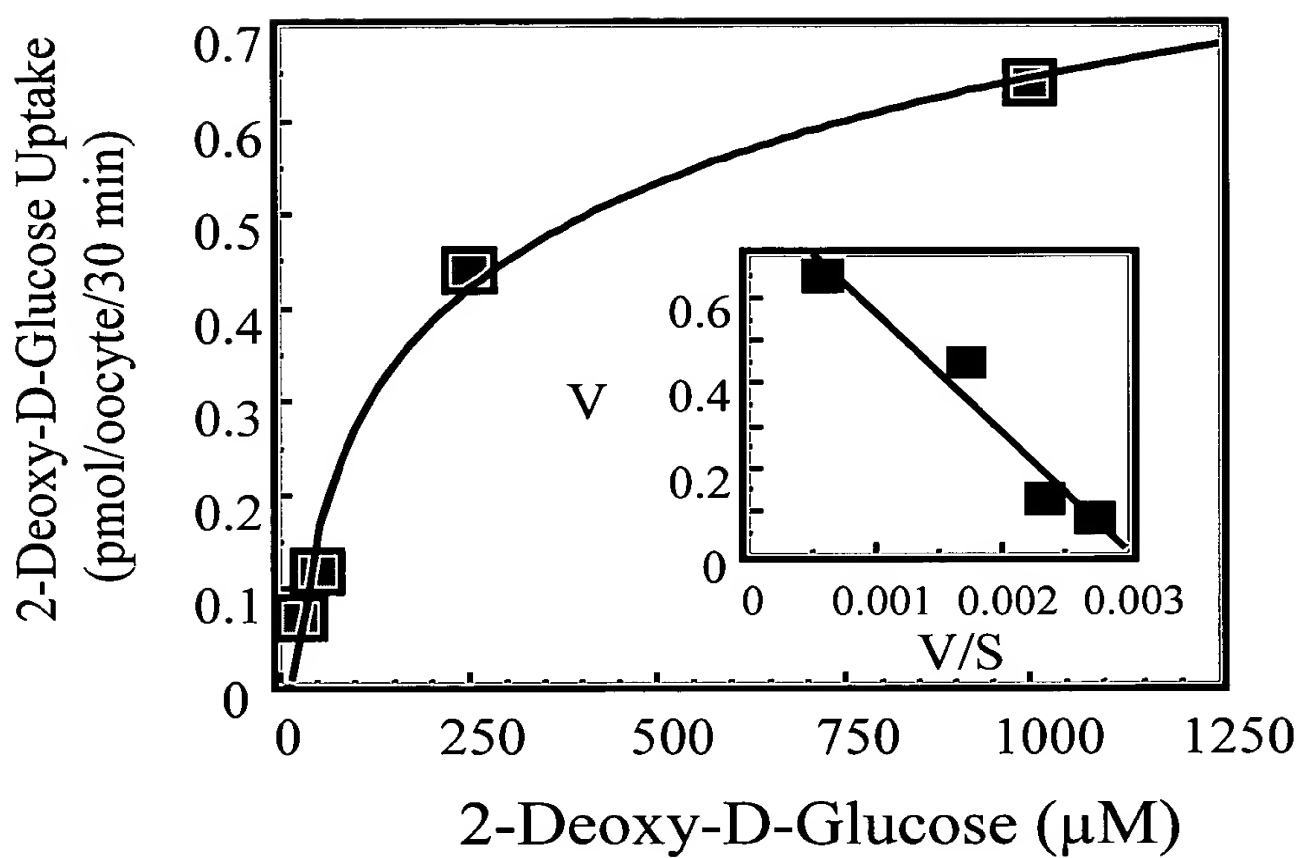


Fig. 6

